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============================================================
Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2007; month=12; day=29; hr=9; min=42; sec=8; ms=156; ]
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Reviewer Comments:
<210>   9
<211>   1421
<212>   DNA
<213>   murine



<220>
<221>   misc_feature
<222>   (40)..(40)
<223>   n = degenefacy in code


<400>   9

   The above "n" response for sequence id# 9 is invalid, please explain
"n" location.
   FYI, "n"s can only represent a single nucleotide.
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Application No: 10559438   Version No: 2.0

Input Set:

Output Set:

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Finished: 2007-12-03 19:59:25.633
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 734 ms
Total Warnings: 86
Total Errors: 0
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started:	2007-12-03 19:59:20.899
Finished:	2007-12-03 19:59:25.633
Elapsed:	0 hr(s) 0 min(s) 4 sec(s) 734 ms
Total Warnings:	86
Total Errors:	0
No. of SeqIDs Defined:	86
Actual SeqID Count:	86

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (22)
W 402	Undefined organism found in <213> in SEQ ID (23)
W 402	Undefined organism found in <213> in SEQ ID (24) This error has occured more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (44)
W 213	Artificial or Unknown found in <213> in SEQ ID (85)

<110> McWhirter, John

<120> CELL SURFACE PROTEIN ASSOCIATED WITH HUMAN CHRONIC LYMPHOCYTIC
       LEUKEMIA

<130> ALEX-P01-107

<140> 10559438
<141> 2007-12-03

<150> US 60/530,094
<151> 2003-12-15

<150> US 60/475,156
<151> 2003-06-02

<160> 86

<170> PatentIn version 3.2

<210> 1
<211> 183
<212> PRT
<213> human

<400> 1

Met Gln Ala Pro Arg Ala Ala Leu Val Phe Ala Leu Val Ile Ala Leu
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Val Pro Val Gly Arg Gly Asn Tyr Glu Glu Leu Glu Asn Ser Gly Asp
            20   25   30

Thr Thr Val Glu Ser Glu Arg Pro Asn Lys Val Thr Ile Pro Ser Thr
        35   40   45

Phe Ala Ala Val Thr Ile Lys Glu Thr Leu Asn Ala Asn Ile Asn Ser
    50   55   60

Thr Asn Phe Ala Pro Asp Glu Asn Gln Leu Glu Phe Ile Leu Met Val
65   70   75   80

Leu Ile Pro Leu Ile Leu Leu Val Leu Leu Leu Leu Ser Val Val Phe
            85   90   95

Leu Ala Thr Tyr Tyr Lys Arg Lys Arg Thr Lys Gln Glu Pro Ser Ser
            100   105   110

Gln Gly Ser Gln Ser Ala Leu Gln Thr Tyr Glu Leu Gly Ser Glu Asn
        115   120   125

Val Lys Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu Ile
     130   135   140

Glu Met Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn Ala
145   150   155   160

Asp Phe Glu Cys Leu Pro Thr Leu Lys Glu Glu Lys Glu Ser Asn His
                165   170   175

Asn Pro Ser Asp Ser Glu Ser
            180

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<213>   human

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ttatgaggaa ttagaaaact caggagatac aactgtggaa tctgaaagac caaataaagt   180

gactattcca agcacatttg ctgcagtgac catcaaagaa acattaaatg caaatataaa   240

ttctaccaac tttgctccgg atgaaaatca gttagagttt atactgatgg tgttaatccc   300

attgatttta ttggtcctct actttttatc cgtggtattc cttgcaacat actataaaag   360

aaaaagaact aacaagaacc ttctagccaa ggatctcaga gtgctttaca gacatatgaa   420

ctgggaagtg aaaacgtgaa agtccctatt tttgaggaag atacaccctc tgttatggaa   480

attgaaatgg aagagcttga taaatggatg aacagcatga atagaaatgc cgactttgaa   540

tgtttaccta ccttgaagga agagaaggaa tcaaatcaca acccaagtga cagtgaatcc   600

taaacctgaa tggcgctcat gttttccaag agaagcagcc cctgagggag tctgctgagg   660

ctgccaacag gatcc   675

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<211>   181
<212>   PRT
<213>   murine

<400> 3

Met Thr Val Pro Cys Ala Ala Leu Val Leu Ala Leu Gly Leu Ala Phe
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Gly Gln Ser Ser Gln Gly Asn Asp Glu Glu Ser Glu Tyr Ser Gly Gln
            20   25   30

Ser Ile Thr Glu Glu Glu Asn Ser Glu Asp Glu Thr Thr Arg Ser Ala
        35   40   45

Leu Ala Thr Val Thr Thr Glu Ala Leu Ala Glu Asn Val Asn Ser Thr
        50   55   60

His Thr Asn Asp Thr Ser Asn Gln Val Glu Phe Ile Leu Met Val Ala
65   70   75   80

Ile Pro Leu Ala Ala Leu Leu Ile Leu Leu Phe Met Val Leu Ile Ala
            85   90   95

Thr Tyr Phe Lys Ser Lys Arg Pro Lys Gln Glu Pro Ser Ser Gln Gly
            100   105   110

Ser Gln Ser Ala Leu Gln Thr His Glu Leu Gly Gly Glu Thr Leu Lys
        115   120   125

Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu Ile Glu Met
        130   135   140

Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn Ala Asp Tyr
145   150   155   160

Glu Cys Leu Pro Thr Leu Lys Glu Glu Lys Glu Pro Asn Pro Ser Pro
                165   170   175

Ser Asp Asn Glu Ser
            180

<210> 4
<211> 367
<212> PRT
<213> rat

<400> 4

Met Thr Arg Pro Pro Tyr Gln Glu Ala Pro Val Gly Asp Leu Gln Met
1   5   10   15

Gly Asp Arg Gln Glu Ser Ser Gly Asp Lys Asp Arg Asn Asp Glu Asp
            20   25   30

Ser Glu Tyr Ser Gly His Ser Thr Thr Glu Glu Asp Thr Ala Glu Glu
        35   40   45

Glu Thr Thr Arg Ala Leu Ala Thr Val Thr Thr Glu Ala Leu Ala Glu
        50   55   60

Ser Ala Asn Ser Thr His Ile His Gly Thr Ser Asn Gln Val Glu Phe
65   70   75   80

Ile Leu Met Val Ala Val Pro Leu Ala Ala Leu Leu Ile Leu Leu Phe
                85   90   95

Ala Ile Leu Ile Val Ile Tyr Phe Lys Ser Arg Arg Pro Lys Gln Glu
                100   105   110

Pro Ser Ser Gln Gly Ser Gln Ser Ala Leu Gln Thr Leu Arg Leu Leu
            115   120   125

Leu Ser Leu Glu Thr Lys Arg Pro Glu Pro Ser Val Ala Pro Ser Leu
            130   135   140

Gly Pro Arg Pro Thr Ile Pro Leu Pro Thr Ala Gln Arg Gly Pro Cys
145   150   155   160

Gln Gln Ser Gly Cys Lys Ala Gly Thr Lys Gly Gly Arg Gln Asp Arg
                165   170   175

Gly Glu Asn Glu Met Ala Gly Arg Lys Gly Thr Lys Trp Lys Pro Val
                180   185   190

Gly Asn Gly Pro Gly Ala Glu Lys Met Arg Pro Gln Lys Ala Phe Cys
            195   200   205

Ser Phe Asn Ala Asp Tyr Gly Ala Ser His Ser Val His Leu Glu His
        210   215   220

Phe Gly Asn Gly Phe Leu Asn Phe Ser Ile Ile Cys Met Gln Val Gly

Phe Cys Pro Pro Pro Ser Leu Trp Gly Ala Gln Met Arg Val Glu Ile
             245   250   255

Arg Ala His Ser Gly Thr Val Glu Pro Leu Ala Val Trp Glu Ile Gly
             260   265   270

Gly Glu Val Ala Lys Gln Gly Lys Gly Thr Asp Asp Leu Gly Gly Glu
          275   280   285

Thr Leu Lys Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu
       290   295   300

Ile Glu Met Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn
305   310   315   320

Gly Thr Trp Lys Thr Lys Ala Phe Ala Cys Leu Cys Gly Asn Ala Gly
             325   330   335

Leu Asp Gly Cys Leu Cys Phe Ile Ser Asn Ser Glu Asn Leu Lys Leu
          340   345   350

Cys Phe Ile Trp His Ser Thr Cys Ala Leu Leu Lys Asp Pro Val
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<212> DNA
<213> artificial sequence

<220>
<223> FLJ32028 with an HA epitope tag

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tgtggaatct gaaagaccaa ataaagtgac tattccaagc acatttgctg cagtgaccat   240

caaagaaaca ttaaatgcaa atataaattc taccaacttt gctccggatg aaaatcagtt   300

agagtttata ctgatggtgt taatcccatt gatttttattg gtcctcttac ttttatccgt   360

ggtattcctt gcaacatact ataaaagaaa aagaactaaa caagaacctt ctagccaagg   420

atctcagagt gctttacaga catatgaact gggaagtgaa aacgtgaaag tccctatttt 480

tgaggaagat acaccctctg ttatggaaat tgaaatggaa gagcttgata aatggatgaa 540

cagcatgaat agaaatgccg actttgaatg tttacctacc ttgaaggaag agaaggaatc 600

aaatcacaac ccaagtgaca gtgaatccta aacctgaatg gcgctcatgt tttccaagag 660

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<211> 192
<212> PRT
<213> artificial sequence

<220>
<223> FLJ32028 with HA epitope tag

<400> 6

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Val Pro Val Gly Arg Gly Asn Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
            20   25   30

Tyr Glu Glu Leu Glu Asn Ser Gly Asp Thr Thr Val Glu Ser Glu Arg
        35   40   45

Pro Asn Lys Val Thr Ile Pro Ser Thr Phe Ala Ala Val Thr Ile Lys
    50   55   60

Glu Thr Leu Asn Ala Asn Ile Asn Ser Thr Asn Phe Ala Pro Asp Glu
65   70   75   80

Asn Gln Leu Glu Phe Ile Leu Met Val Leu Ile Pro Leu Ile Leu Leu
                85   90   95

Val Leu Leu Leu Leu Ser Val Val Phe Leu Ala Thr Tyr Tyr Lys Arg
            100   105   110

Lys Arg Thr Lys Gln Glu Pro Ser Ser Gln Gly Ser Gln Ser Ala Leu
        115   120   125

Gln Thr Tyr Glu Leu Gly Ser Glu Asn Val Lys Val Pro Ile Phe Glu
    130   135   140

Glu Asp Thr Pro Ser Val Met Glu Ile Glu Met Glu Glu Leu Asp Lys
145   150   155   160

Trp Met Asn Ser Met Asn Arg Asn Ala Asp Phe Glu Cys Leu Pro Thr
                165   170   175

Leu Lys Glu Glu Lys Glu Ser Asn His Asn Pro Ser Asp Ser Glu Ser
                180   185   190

<210>   7
<211>   637
<212>   DNA
<213>   artificial sequence

<220>
<223>   FLJ32028 with HA epitope tag

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tccccgcgca gccctagtct tcgccctggt gatcgcgctc gttcccgtcg ccggggtaa   120

ttatgaggaa ttagaaaact caggagatac aactgtggaa tctgaaagac caaataaagt   180

gactattcca agcacatttg ctgcagtgac catcaaagaa acattaaatg caaatataaa   240

ttctaccaac tttgctccgg atgaaaatca gttagagttt atactgatgg tgttaatccc   300

attgatttta ttggtcctct tactttatc cgtggtattc cttgcaacat actataaaag   360

aaaaagaact aaacaagaac cttctagcca aggatctcag agtgctttac agacatatga   420

actgggaagt gaaaacgtga aagtccctat ttttgaggaa gatacaccct ctgttatgga   480

aattgaaatg gaagagcttg ataaatggat gaacagcatg aatagaaatg ccgactttga   540

atgtttacct accttgaagg aagagaagga atcaaatcac aacccaagtg acagtgaatc   600

ctatccatat gatgttccag attatgctta aggatcc   637

<210>   8
<211>   192
<212>   PRT
<213>   artificial sequence

<220>
<223>   FLJ32028 with HA epitope tag

<400>   8

Met Gln Ala Pro Arg Ala Ala Leu Val Phe Ala Leu Val Ile Ala Leu
1   5   10   15

Val Pro Val Gly Arg Gly Asn Tyr Glu Glu Leu Glu Asn Ser Gly Asp
            20   25   30

Thr Thr Val Glu Ser Glu Arg Pro Asn Lys Val Thr Ile Pro Ser Thr
            35   40   45

Phe Ala Ala Val Thr Ile Lys Glu Thr Leu Asn Ala Asn Ile Asn Ser
    50   55   60

Thr Asn Phe Ala Pro Asp Glu Asn Gln Leu Glu Phe Ile Leu Met Val
65   70   75   80

Leu Ile Pro Leu Ile Leu Leu Val Leu Leu Leu Leu Ser Val Val Phe
                85   90   95

Leu Ala Thr Tyr Tyr Lys Arg Lys Arg Thr Lys Gln Glu Pro Ser Ser
                100   105   110

Gln Gly Ser Gln Ser Ala Leu Gln Thr Tyr Glu Leu Gly Ser Glu Asn
            115   120   125

Val Lys Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu Ile
            130   135   140

Glu Met Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn Ala
145   150   155   160

Asp Phe Glu Cys Leu Pro Thr Leu Lys Glu Glu Lys Glu Ser Asn His
                165   170   175

Asn Pro Ser Asp Ser Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
                180   185   190

<210>   9
<211>   1421
<212>   DNA
<213>   murine

<220>
<221>   misc_feature
<222>   (40)..(40)
<223>   n = degenefacy in code

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acctgcagaa accaggccag tctccaaagc tcctgatcta caaagtttcc aaccgatttt   180

ctggggtccc agacaggttc agtggcagtg gatcagggac agatttcaca ctcaagatca   240

gcagagtgga ggctgaggat ctgggagttt attactgctt tcaaggttca catgttccgc   300

tcacgttcgg tgctgggacc aagctggagc tgaaacgggc tgatgctgca ccaactgtat   360

ccatcttccc accatccagt gagcagttaa catccggagg tgcctcagtc gtgtgcttct   420

tgaacaactt ctaccccaaa gacatcaatg tcaagtggaa gattgatggc agtgaacgac   480

aaaatggcgt cctgaacagt tggactgatc aggacagcaa agacagcacc tacagcatga   540

gcagcaccct cacgttgacc aaggacgagt atgaacgaca taacagctat acctgtgagg   600

ccactcacaa gacatcaact tcacccattg tcaagagctt caacaggaat gagtgttaag   660

cggccgcact agatataatt aaggagataa atatgaaata tctgctgccg accgcggcgg   720

cgggcctgct gctgctggcg gcgcagccgg cgatggcgct cgaggtgaag ctggtggagt   780

ctggggggagg cttagtgaag cctggagggt ccctgaaact ctcctgtgca gcctctggat   840

tcactttcag tgactatgcc atgtcttggg ttcgccagac tccagagaag aggctggagt   900

gggtcgcatc aattagtagt ggtggtacca cctattatct agacagtgtg aagggccgat   960

tcaccatctc cagagataat gccaggaaca tcctgtacct gcaaatgagc agtctgaggt   1020

ctgaggacac ggccatgtat tattgtgtaa gaagtgagac gaactactgg ggccaaggca   1080

ccactctcac agtctcctca gccaaaacga cacccccatc tgtctatcca ctggcccctg   1140

gatctgctgc ccaaactaac tccatgataa ccctaggctg cctggtcaag gactacttcc   1200

ccgaaccggt gacggtgtcg tggaactcag cgctctgac cagcggcgtg cacaccttcc   1260

cggctgtcct acagtcctca ggactctact ccctcagcag cgtggtgacc gtgccatcca   1320

gcagcttggg cacccagacc tacatctgca acgtgaatca caagcccagc aacaccaagg   1380

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<210> 10
<211> 474
<212> PRT
<213> murine

<220>

<400> 10

Tyr Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Xaa Phe Gly
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Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
            20   25   30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
                85   90   95

Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105   110

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
        115   120   125

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
    130   135   140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
145   150   155   160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
                165   170   175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
            180   185   190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
        195   200   205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Xaa Ala Ala Ala Leu
        210   215   220

Asp Ile Ile Lys Glu Ile Asn Met Lys Tyr Leu Leu Pro Thr Ala Ala
225   230   235   240

Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Leu Glu Val
        245   250   255

Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu
        260   265   270

Lys Leu Ser Cys